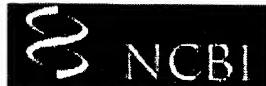


seq 33

seq 23



# Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

## BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.17 [Aug-26-2007]

Match: 1 Mismatch: -2 gap open: 5 gap extension: 2

x\_dropoff: 0 expect: 10.0000 wordsize: 11 Filter  View option Standard

Masking character option X for protein, n for nucleotide  Masking color option Black

Show CDS translation

**Align**

### Sequence 1: lcl|1

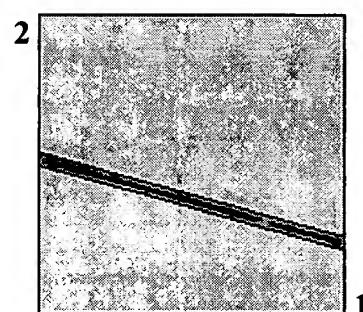
Length = 529 (1 .. 529)

Instant seq ID NO: 33

### Sequence 2: lcl|65536

Length = 1895 (1 .. 1895)

Instant seq ID NO: 23



Alignment 1  
part of Paper No: 20080103

NOTE: Bitscore and expect value are calculated based on the size of the nr database.

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

Score = 1017 bits (529), Expect = 0.0  
Identities = 529/529 (100%), Gaps = 0/529 (0%)  
Strand=Plus/Minus

Query 1	TTTGGTTTCTCCAGTAGGAGTTCTCATCATATATTCTATTCTATTCTATTCTGGG	60
Sbjct 982	TTTGGTTTCTCCAGTAGGAGTTCTCATCATATATTCTATTCTATTCTATTCTGGG	923
Query 61	CTGATCGAATGAGCTCCTGGATGTTCTCATTATCATAGGAGTAGACTCTACTTCTCGTA	120
Sbjct 922	CTGATCGAATGAGCTCCTGGATGTTCTCATTATCATAGGAGTAGACTCTACTTCTCGTA	863
Query 121	CCCGGGGAGCAAAAGAGGAAGGGTTAGAAGATAGAGATTAGAGTGAAACTGGGCTCTG	180

Sbjct	862	CCCGGGGAGCAAAAGAGGAAGGGTTAGAAGATAGAGATTAGAGTGAACATTGGGCTCTG	803
Query	181	AGTCTGTCAGCTGAGACACAGCCTCCGTCCCTCCTTAGTCCCCTGTCCTTCTCCT	240
Sbjct	802		743
Query	241	GCTTCCCTCCTCTCCTGTTCCCTTTGCTCTCCTGTTCTGCCCTCTCCTGCT	300
Sbjct	742		683
Query	301	TGTGTTCTTGTGTCGGCTCCTGCCTGTGCTCCACTCCTGCTCCTGCTTGTGCTCTGGCG	360
Sbjct	682		623
Query	361	CTTGCTCCTGGCCTCCCAGGGACAAGGAGGATTGTTAGGAGCTTCCACGTTGCTGA	420
Sbjct	622		563
Query	421	GCCTCTCAGGCCAGGGCTGGAAGGTCTGGCGTTCTGTCACTGTGAAGTGGGTGAGATGG	480
Sbjct	562		503
Query	481	GGGAGGTACCGTGGTGGGTGAGACTTCAGCTGAAGCTTCTATCTCCTT	529
Sbjct	502		454

CPU time: 0.05 user secs. 0.03 sys. secs 0.08 total secs.



# Blast 2 Sequences results

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Structure

## BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.17 [Aug-26-2007]

Match: 1 Mismatch: -2 gap open: 5 gap extension: 2

x\_dropoff: 0 expect: 10.0000 wordsize: 11 Filter  View option Standard

Masking character option X for protein, n for nucleotide  Masking color option Black

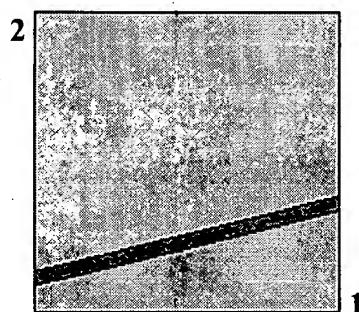
Show CDS translation  Align

**Sequence 1:** lcl|1  
Length = 460 (1 .. 460)

Jacobs Seg Id 11

**Sequence 2:** lcl|65536  
Length = 1895 (1 .. 1895)

Instant Seg Id 23



Alignment 2  
part of Paper No. 20080103

NOTE: Bitscore and expect value are calculated based on the size of the nr database.

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

Score = 885 bits (460), Expect = 0.0  
Identities = 460/460 (100%), Gaps = 0/460 (0%)  
Strand=Plus/Plus

Query 1	GCCGTCTCCGTGCAACCCACGGCTGCCGAATCCCACACTCGTCCAGCTGGACCAATATG	60
Sbjct 227	GCCGTCTCCGTGCAACCCACGGCTGCCGAATCCCACACTCGTCCAGCTGGACCAATATG	286
Query 61	AAAACCACGGCTTAGTGCCCGATGGTGTCTGCTCCAACCTCCATTGCCTCCTGGT	120
Sbjct 287	AAAACCACGGCTTAGTGCCCGATGGTGTCTGCTCCAACCTCCATTGCCTCCTGGT	346
Query 121	TTGAGTCTTCTGCCAGTTCACTCACTACCGTTGCTCCAACCACGTCTACTATGCCAAGA	180

Sbjct	347	TTGAGTCTTCTGCCAGTTCACTCACTACCGTTGCTCCAACCACGTCTACTATGCCAAGA	406
Query	181	GAGTCCTGTGTTCCCAGCCAGTCTCTATTCTCACCTAACACTCTCAAGGAGATAGAAG	240
Sbjct	407	GAGTCCTGTGTTCCCAGCCAGTCTCTATTCTCACCTAACACTCTCAAGGAGATAGAAG	466
Query	241	CTTCAGCTGAAGTCTCACCCACCACGATGACCTCCCCATCTCACCCACTTCACAGTGA	300
Sbjct	467	CTTCAGCTGAAGTCTCACCCACCACGATGACCTCCCCATCTCACCCACTTCACAGTGA	526
Query	301	CAGAACGCCAGACCTTCCAGCCCTGGCCTGAGAGGCTCAGCAACAAACGTGGAAGAGCTCC	360
Sbjct	527	CAGAACGCCAGACCTTCCAGCCCTGGCCTGAGAGGCTCAGCAACAAACGTGGAAGAGCTCC	586
Query	361	TACAATCCTCCTTGCCCTGGGAGGCCAGGAGCAAGCGCCAGAGCACAAGCAGGAGCAAG	420
Sbjct	587	TACAATCCTCCTTGCCCTGGGAGGCCAGGAGCAAGCGCCAGAGCACAAGCAGGAGCAAG	646
Query	421	GAGTGGAGCACAGGCAGGAGCCGACACAAGAACACAAGCA	460
Sbjct	647	GAGTGGAGCACAGGCAGGAGCCGACACAAGAACACAAGCA	686

CPU time: 0.03 user secs. 0.03 sys. secs 0.06 total secs.



## Blast 2 Sequences results

PubMed

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Structure

### BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.17 [Aug-26-2007]

Match: 1 Mismatch: -2 gap open: 5 gap extension: 2

x\_dropoff: 0 expect: 10.0000 wordsize: 11 Filter  View option Standard

Masking character option X for protein, n for nucleotide  Masking color option Black

Show CDS translation

**Align**

**Sequence 1:** gi|22619253|5'EST of secreted protein expressing in testis and other tissues

Length = 128 (1 .. 128)

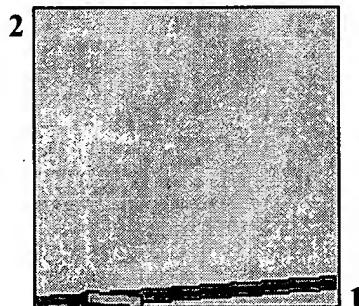
**Sequence 2:** lcl|65536

Length = 1895 (1 .. 1895)

Dumas Milne Edwards SEQ ID NO:60

Instant SEQ ID NO:23

+



Alignment 3  
part of Paper No. 20080103

NOTE: Bitscore and expect value are calculated based on the size of the nr database.

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

+

Score = 237 bits (123), Expect = 9e-60  
Identities = 125/126 (99%), Gaps = 0/126 (0%)  
Strand=Plus/Plus

Query	2	GGGCGGATCTTCTCGGCCATGAGGAAGCCAGCCGCTGGCTTCCTCCCTCACTCCTGAA	61
Sbjct	30	GGGCGGATCTTCTCGGCCATGAGGAAGCCAGCCGCTGGCTTCCTCCCTCACTCCTGAA	89
Query	62	GGTGCTGCTCCTGCCCTGGCACCTGCCGAGCCCAGGATTGACTCAGGCCTCCACTCC	121
Sbjct	90	GGTGCTGCTCCTGCCCTGGCACCTGCCGAGCCCAGGATTGACTCAGGCCTCCACTCC	149
Query	122	AGGCAG 127	

Sbjct 150 AGGCAG 155

—  
—

Score = 39.1 bits (20), Expect = 3.9  
Identities = 22/23 (95%), Gaps = 0/23 (0%)  
Strand=Plus/Minus

Query 24 AGGAAGCCAGCCGCTGGCTTCCT 46  
||||| ||||| ||||| ||||| |||||  
Sbjct 74 AGGAAGCCAGCGGCTGGCTTCCT 52

CPU time: 0.05 user secs. 0.05 sys. secs 0.10 total secs.